

Appendix A

Clustal V alignment of the amino acid sequences having SEQ ID NOs:2, 4, and 6 in the instant application with the cobalamin independent methionine synthases from *E. coli* (NCBI gi No. 836660), *Catharanthus roseus* (NCBI gi No. 1362086), *Coleus blumei* (amino acids 21-84, NCBI gi No. 974782), *Arabidopsis thaliana* (NCBI gi No. 2738248), *Mesembryanthemum crystallinum* (NCBI gi No. 1814403), *Arabidopsis thaliana* (NCBI gi No), and *Solanum tuberosum* (NCBI gi No. 8339545). Amino acids conserved among all the sequences are indicated by an asterisk (*) below the alignment and those conserved only among the plant sequences are indicated by a plus sign (+). The conserved domain containing the active site cysteine (corresponding to *E. coli* 726) is shown boxed.

	1	60
836660	MTILNHTLGFPVGLRRELKKAQESYWAGNSTREELLAVGRELRARHWDQQKQAGIDLLP	
1362086	MA--SHIVGYPRMGPKRELKFALESFWDKKSSAEDLQKVAADLRSSIWKQMADAGIKYIP	
SEQIDNO02	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLEKVATDLRSSIWKQMSEAGIKYIP	
SEQIDNO04	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLQKVAADLRSSIWKQMAGAGIKYIP	
SEQIDNO6	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLKKVAADLRSSIWKQMADAGIKYIP	
8439545	MA--SHVVGYPYPRMGPKRELKFALESFWDGKSSAEDLKKVSADLRSSIWKQMSDAGIKYIP	
CAA89019	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLEKCQLILGIHL-KQMSDAGIKYIP	
AAB41896	MA--SHIVGYPRMGPKRELKFALESFWDGKSTAEDLKKVSADLRSSIWKQMADAGIKYIP	
2738248	MA--SHIVGYPRMGPKRELKFALESFWDGKSTAEDLQKVSADLRSSIWKQMSAAGTKFIP	
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	61	120
836660	VGDFAWYDHVLTTSLLLGNVPARHQNKDGSVDIDTLFRIGRGRAPTGEPA	AAAAEMTKWFN
1362086	SNTFSYYDQVLDTATMLGAVPPRYNFAGGEIGFDITYFSMARGNASV---	PAMEMTKWFD
SEQIDNO02	SNTSSYYDQVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATV---	PAMEMTKWFD
SEQIDNO04	SNTFSFYDQLLDATATLGAVPPRYGWTGGEIGFDITYFSMARGNATV---	PAMEMTKWFD
SEQIDNO6	SNTFSYYDQVLDTTAMLGAVPARYNWAGGEIAFDITYFSMARGNASV---	PAMEMTKWFD
8439545	SNTFSYYDQVLDTTAMLGAVPSRYNWTGGEIEFGTYFSMARGNASV---	PAMEMTKWFD
CAA89019	SNTFSYYDQVLDTTAMLGAVPPRYNWTGGEIGFSTYFSMARGNASV---	PAMEMTKWFD
AAB41896	SNTFSYYDQVLDTTAMLGAVPPRYGWTGGEIEFDVYFSMARGNASV---	PAMEMTKWFD
2738248	SNTFAHYDQVLDTTAMLGAVPPRYGYTGGEIGLDVYFSMARGNASV---	PAMEMTKWFD
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	121	180
836660	TNYHYMVPEFVKGQQFKLTWTQLLDEVDEALALGHKVKPVL	LGPVTWLWL GK-VKGEQ-
1362086	TNYHYIVPELGPEVNF	SYASHKAVNEYKEAKELGVD
SEQIDNO02	TNYHFIVPELG	PSTKFTYASHKAVSEYKEAKALGID
SEQIDNO04	TNYHFIVPELGPDVNF	TXASQKAVDEYKEAKALGVD
SEQIDNO6	TNYHFIVPELGPDVNF	SYASHKAVDEYKEAKGLGVD
8439545	TNYHFIVPELGPDVNF	SYASHKAVNEYKEAKAQGV
CAA89019	TNYHFIVPELGPDVKF	SYASHKAVNEYKEAKALGVD
AAB41896	TNYHFIVPELGPEVNF	SYASHKAVLEYKEAKALGVD
2738248	TNYHYIVPELGPEVNF	SYASHKAVNEYKEAKALGVD
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181 240
836660 FDRLSLLNDILPVYQQVLAELAKRGIEWVQIDEPALVLELPQAWLDAYKPAYDALQGQV-
1362086 FPLLSLLDKILPVYKEVIGELKAAGASWIQFDEPTLVLDLESHQLEAFTKAYSELESTLS
SEQIDN002 FSLLSLLGSILPIYKEVVAELKAAGASWIQFDEPTLVKDLDHAELAASFSSAYAELESSFS
SEQIDN004 FSLLSLLPKVLAVYKEVIADLKAAGASWIQFDEPTLVLDLESHKLQAFDAYAELAPALS
SEQIDN06 FPLLSLLDKVLPYKEVIAELKAAGASWIQFDEPTLVLDLQAHQLEAFTKAYAELESSLS
8439545 FPLLSLLDKILPIYKEVIAELKAAGASWIQFDEPTLVLDLESHKLEAFTKAYADLESSLS
CAA89019 FPLLSLLDKILPIYKEVIAELKAAGASWIQFDEPTLVLDLESHQLDAFTKAYAELESSLS
AAB41896 FDLSLLPKILPIYKEVVAELKEAGASWIQFDEPLLVMDLESHKLQAFSAAYADLESTLS
2738248 FELSLLPKILPIYKEVITELKAAGATWIQFDEPLVMDLEGQKLQAFDAYAELESTLS
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241 300
836660 --KLLTTYFEGVTPN-LDTITALP-VQGLHVDLVHGKDDVAELHKRLPSDWLLSAGLIN
1362086 GLNVIVETYFADIPAETYKILTALKGVTGFGFDLVRGAKTLDLIKGGFSPSGKYLFAGVVD
SEQIDN002 GLNVLITYFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSFPSGKYLFAGVVD
SEQIDN004 DLNVLVETYFADIPAAYKTLTSLNGVTAYGFDLVRGHTTLDLIKGGFSPSGKYLFAGVVD
SEQIDN06 GLNVLITYFADVPAAEFKTLTALKGVTAFGFDLVRGAQTLDLIKGGFSPSGKYLFAGVVD
8439545 GLNVLVETYFADVPAAEFKTLTALKGVTAFGFDLVRGTQTLELIKSSFPSGKYLFAGVVD
CAA89019 GLSTLITYFADVPAPAYKTLTSLSGISGFGFDLVRGAQTIELIKGGFSPSGKYLFAGVVD
AAB41896 GLNVVVETYFADVTAAYKTLISLKGVTGYGFDLVRGTKTLDLVKAEPSPSGKYLFAGVVD
2738248 GLNVLVETYFADIPAAYKTLTSLKGVTAFGFDLVRGTKTLDLVKAGFPEGKYLFAGVVD
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301 360
836660 GRNVWRADLTEKYAQIKD--IVGKRDLWVASSCSLLHSPIDLSVETRLDAEVKSWFAFA
1362086 GRNIWANDLAASLSTLQSLEGIVGKDKLVVSTSCSLLHTAVDLVNEPKLDKEIKSWLAFA
SEQIDN002 GRNIWADDLAASLSTLHSLEAVAGKDKLVVSTSCSLMHTAVDLVNETKLDDEIKSWLAFA
SEQIDN004 GRNIWANDLAASLTTLQGLEGIVGKDKLVVSTSSSLLHTAVDLVNETKLDDEIKSWLAFA
SEQIDN06 GRNIWANDLAASLNLQSLEGIVGKDKLVVSTSCSLLHTAVDLVNETKLDDEIKSWLAFA
8439545 GRNIWANDLAASLALLQSLEGVVGKDKLVASTSCSLLHTAVDLINETKLDDEIKSWLAFA
CAA89019 GRNIWANDLASSITTLQALEGIVGKDKLVVSTSSSLLHTAVDLVNEPKLDQEIKSWLAFA
AAB41896 GRNIWANDLAASLATLEAGVVGKDKLVVSTSCSFLHTAVDLINETKLDDEIKSWLAFA
2738248 GRNIWANDFAASLSTLQALEGIVGKDKLVVSTSCSLLHTAVDLINETKLDDEIKSWLAFA
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361 420
836660 LQKCHELALLRDALNSGDTAAL-AEWSAPIQARRHSTRVHNPAVEKRLAAITAQDSQRAN
1362086 AQKVVEVNALAKALAGEKDEAFFSENAQAASRKSSPRVTNQAVQKAAAALRGSDHRRAT
SEQIDN002 AQKVVEVNALAKALAGQKDEVYFAANAAAQASRRSSPRVTNEEVQKAAAALRGSDHRRST
SEQIDN004 AQKIVEVNALAKALSGNKDVAFSSANAAAQASRKSSPRVTNEAVQKAAAALKGSDHRRAT
SEQIDN06 AQKVVEVNALAKALAGHKDEAFFSANATAQASRKSSPRVTNEAVQKAAAALKGSDHRRAT
8439545 AQKVVEVNALAKALSGAKDEAFFSANAAAQASRKSSPRVTNEAVQKASAAALQGS DHRRAT
CAA89019 AQKIVEVNALAKALTGHKDEAFFSPNAAAQASRKSSPRVNNEAVQKAAAALRGSEHRRVT
AAB41896 AQKVLEVNALAKALSGQKDEAFFSANAAALASRKSSPRVTNEAVQKAATALKGSDHRRAT
2738248 AQKVVEVNALAKALAGQKDEALFSANAAALASRRSSPRVTNEGVQKAAAALKGSDHRRAT
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	421	480
836660	VYEVRAEAQRARFKLPWPPTTTIGSFPQTTEIRTLRLDFKKGNLDDANNYRTGIAEHKQA	
1362086	TVSARLDAQQKKLNLVPLPTTTIGSFPQTLELRRVRREYKAKKISEDDYVKAIKEEISKV	
SEQIDNO02	TVSARLDAQQKKLNLVPLPTTTIGSFPQTVELRRVRREYKAKKITEDEYISAIKEEISKV	
SEQIDNO04	NVSARLDAQQKKLNLPLPPTTTIGSFPQTVELRRVRREFKANKISEEEYVKSIIKEEIRKV	
SEQIDNO6	NVSSRLDAQQKKLNLVPLPTTTIGSFPQTVELRRVRREYKAKKISEEEYVKAIIKAEIKKV	
8439545	NVSARLDAQQKKLNLPLPPTTTIGSFPQTVELRRVRREYKAKKISEEEYVKAITEEIKKV	
CAA89019	NVSARLDAQQKKLNLPLPPTTTIGSFPQTVELRRVRREFKPTRISEEEYVKAIKEEINKV	
AAB41896	TVSSRLDAQQKKLNLPLPPTTTIGSFPQTVELRRVRREYKAKKISEEEYVKAIKEEISKV	
2738248	NVSARLDAQQKKLNLPLPPTTTIGSFPQTVELRRVRREYKAKKVSEEDYVKAIKEEIKKV	
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	541	600
836660	PAPITVEWAKYAQSLTDKPVKGMLTGPVTILCWSFPREDVSRETI	AKQIALALRDEVADL
1362086	PNPMTVFWSQTAQSMTKRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKDEVEDL	
SEQIDNO02	PNPMTVFWSKMAQSMTPRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKKEVEDL	
SEQIDNO04	PKPMTVFWSSLAQSFTKRPMKGMLTGPVTILNWSFVRNDQPRSETTYQIALAIKDEVEDL	
SEQIDNO6	PNPMTVFWSKTAQSMTKRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKDEVEDL	
8439545	PKPMTVFWSSKAQEMTKRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKDEVEDL	
CAA89019	PKPMTVFWSTAAQSMTQRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKDEVEDL	
AAB41896	PNPMTVFWSSMAQSMTARPMKGMLTGPVTILNWSFVRNDQPRHETCYQIALAIKNEVEDL	
2738248	PKAMTVFWSAMAQSMTSRPMKGMLTGPVTILNWSFVRNDQPRHETCYQIALAIKDEVEDL	
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	661	720
836660	DIMDSIAALDRDVITIETSRSDMELLESF-EEFDYPNEIGPGVYDIHSPNVPSVEWIEAL	
1362086	DIIHSIIDMDADVMTIENSRSSEKLLSVFREGVKYAGIGPGVYDIHSPRI PSTEEIADR	
SEQIDNO02	DIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRI PSTEEIADR	
SEQIDNO04	DIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRI PPTEEIADR	
SEQIDNO6	DIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRI PSTEEIADR	
8439545	DIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRI PSTEEIADR	
CAA89019	DIIHSIINMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRI PSTEEIADR	
AAB41896	DIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRI PPTEELADR	
2738248	DIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRI PSSEEIADR	
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